



FIGURE 1A

SEQ ID NO: 41	M-----GHGGE-----GMSLEFPTTWVAGVCTVIVALSIAVERLLH	60
SEQ ID NO: 40	MITRSRCRSLWFLVFHGGATATCAPSGGKELSTQPTWAVAVVCTFLILISHLEKGLQ	
SEQ ID NO: 39	M-----SDRKG--VPARELPETPSWAVAVFAAVLVSVLMEHGLH	
SEQ ID NO: 42	M-----ADQ---VKEKTEETSTWAVAVGVFLLISIVIEKLIH	
SEQ ID NO: 08	M-----SGGGE-----GATLEFPTTWVAAFCTVIVALSIAAERLLH	
SEQ ID NO: 12	M-----AGESSSSRDLDQPTWAVAVVCTVILVSIKLESLH	
SEQ ID NO: 14	M-----GGGGE-----GNNLEFPTTWVAVCVSVIVAAAFERFLH	
SEQ ID NO: 28	M-----KTIQETPTWAVAVGVFLLISILIEHILH	
SEQ ID NO: 32	M-----AEDYEYPPARTTPETPSWAVAVFAVMIIVSVILLEHALH	
SEQ ID NO: 38	M-----AGGGK-----AKPLEYPTTWIVALVCSVMIIISLLFERLLH	60
	1	
SEQ ID NO: 41	YFGTVLKKKQKPLYEALQVKKEIMLLGFISLLLTVFQGL--ISKFCVKENVLMHMLPCS	
SEQ ID NO: 40	RLANWLKKHRNLSLEALEKIKAEIMILGFISLLLTTFGE--PYILKICVPRKAALSMPLCL	
SEQ ID NO: 39	KLGHWFQHRHKKALWEALEKMKAEIMLVGFISLLLTITQDPIIAKICISEDAADVMWPK	
SEQ ID NO: 42	KIGSWFKKKNKALYEALKEVKAEIMLMGFISLLLTIGOG--YISNICIPKNIASMHSPCS	
SEQ ID NO: 08	YGGKFLKAKDQKPLYEALQKKEIMLLGFISLLLTITONG--ITKICVRPSLTLMHMLPCN	
SEQ ID NO: 12	KVGTWLGQKKKALLEALEKVKAEIMILGFISLLLTTFGO--SYIVRICIPEKLADNMLPCP	
SEQ ID NO: 14	YGGKFLKKNQKPLYEALKEIKAEIMLLGFISLLLTITONG--IIRICVPGVGTWHMLPCPS	
SEQ ID NO: 28	LIGKWLKKKKRALCEALEKIKAEIMLLGFISLLLTITONG--LISRICISEKVAFTFHPCP	
SEQ ID NO: 32	KLGHWFHKKRKNALAEALEKIKAEIMLVGFISLLLTAVTQDPSG--ICISEKAASIMRPPCS	
SEQ ID NO: 38	RLGKRLIRSRKKPLYEALIKVKEIMLLGFISLLLTVFQCP--MGKVCVSPSAMLHLQPCK	120
	61	



FIGURE 1B

SEQ ID NO: 41 LDSR-----REAGASEHKNVTAKHEHFOFELPIVG--TTRRLIAEH-----AAVQVGCSEK  
SEQ ID NO: 40 -----SEDTVLFOKLAPSSL-----SRHLLAAGDTSIN-----C-KQ  
SEQ ID NO: 39 RGTGRK-----PSKYVDI-----CPE-  
SEQ ID NO: 42 ASEEARLYGKKDVPKEDEENLRKLLQLVDS--LIPRRSLATGYD-K-----CAEK  
SEQ ID NO: 08 LHD-----APANES-----HFQTFEP--G--TARRLLSGEHSHPESASKIGYCSRK  
SEQ ID NO: 12 Y-----KY-KEDKKASDSEEHRRKLLSY-----ERRYLAADTTSFK-----CSRE  
SEQ ID NO: 14 I-----KYYKKKEESEHRTNNGRRLLAFLDSNQNHRRILAAAGGD-N-----CPP-  
SEQ ID NO: 28 LPPGSVK-----SKYDYY-----CAKK  
SEQ ID NO: 32 -----PPPHETDHLGD-----AVFTGVLG--GARRLLAGGASSDK-----YCLKK  
SEQ ID NO: 38 -----121  
SEQ ID NO: 41 GKVPLLSLEALHHLHIFIFVLAI SHVTECVLTIVFGSTRIGHQWKWEDSIADKEDPETA  
SEQ ID NO: 40 GSEPLITLKGHLHQLHLLFFFLAIFHIVYSLITMMLSLKIRGWKKWEQETLSNDYFES ID  
SEQ ID NO: 39 GKVALMSTGSLHQLHVFI FVLAVFHVTYSVITIALSKRMRTWKWKWETTTSLYQFAND  
SEQ ID NO: 42 GKVAFSAYGMHQLHIFIFVLAVCHVICYIVTVALGKTKMRWKWKEBETKTIEYQYSHD  
SEQ ID NO: 08 HKVPFLSVEALHHLHIFIFVLAVHVSFSLTVVFGGARIRQWKWEDSIARQNYETDRV  
SEQ ID NO: 12 GHEPLLSVNGHLHILIRLLAVTHLVLSAITMMLGLKILGWKAEAGLQLHNYEFANA  
SEQ ID NO: 14 -----  
SEQ ID NO: 28 GKVPFVSSEGIHQLHIFIFVLAVFHVLYCILTALGAKMRWRKWESETTKTAQYQFSHD  
SEQ ID NO: 32 GKVSLMSTGSLHQLHIFIFVLAVFHVTYSVITIALSKRMRTWKWKWETTTSLYQFAND  
SEQ ID NO: 38 DKVPLSSDAIHQLHIFIFVLAVTHFLLSAITVLLGNAQTNRNRHWETKIQENNGSAPQM  
181 240



FIGURE 1C

SEQ ID NO: 41 LRKRRVTHVNHAFIKEHFLGIGKDSVILGWTSFLKQFYDSVTKSDVYVTLRLGFIIMTH-  
SEQ ID NO: 40 HSRRLRTH--ETSFVREHT-SFWTTTPEFFVVGCFRQFVSVERTDYLTIRHGFISAHL  
SEQ ID NO: 39 PARFRFTH--QTSFVKRHL-GLSSTPGIR-WVAFFRQFRSVTKVDYLTIRAGFINAHL  
SEQ ID NO: 42 PERFRFAR--DTSFGRRLH-SFWSKSTITLWVCFRQFRSVTKVDYLTIRHGFIMAH  
SEQ ID NO: 08 L-KFKVQVHQHDFIRGRFAGFGKDSAIVGWLISFLKQFYGSVTKSDVYVTLRHRGFIMTH-  
SEQ ID NO: 12 ASKTKLIM--ETSFVRSPI-QELIRPIFFYRCFRQFRSVNRTDYLTIRNGEFTIVHL  
SEQ ID NO: 14 -----  
SEQ ID NO: 28 PERFRFAR--ETSFGRRLH-SFAQNPVLLWVCFRQFRSVTKVDYLTIRHGFMAHL  
SEQ ID NO: 32 PARFRFTH--QTSFVKRHL-GLSSTPGIR-WVAFFRQFRSVTKVDYLTIRAGFINAHL  
SEQ ID NO: 38 IK-----HVQEFKIQDHEKGRKRSRIFGWMRSFFKQLYGSVTEEDYVTLRLGFIIMTH-  
241

300

SEQ ID NO: 41 -CKGNPKLNPHKYMRALEDDEKQVVGISVYLWIFVVIPELLNVNGWHTYFWIAFIPAL  
SEQ ID NO: 40 APGR--KFNQRYIKRSLEDDFKLVVGISVPLWASVFIPELLNVNGWRTLFWASIPILLI  
SEQ ID NO: 39 SQNS--KFDFHKYIKRSMEDDFKVVVGISPLMGVAILTFLDINGVGTLIWISFIPVI  
SEQ ID NO: 42 APGSDARDFDKYIQRSLEDFKTIVEINPVIMFIALVFLLLTNTGLNSYLLWLPFIPVI  
SEQ ID NO: 08 -CRTNPKFNPHKYMRALEDDEKQVVGISWDLWLFWVIFLLINNGWHTYFWIAFIPVIL  
SEQ ID NO: 12 APGS--KFNFPKYIKRSLEDDFKVVVGISVPLWASVYVLLNVNGWHTVLAALIPVI  
SEQ ID NO: 14 -----  
SEQ ID NO: 14 GPHSHPKDFPROYIKRSLEDFKVVVR--  
SEQ ID NO: 28 -----  
SEQ ID NO: 32 SHNS--KFDFHKYIKRSMEDDFKVVVGISPLMGVAILTFLDIDIGTGLTWISFIPVI  
SEQ ID NO: 38 -CKGTPKFNYSIMRALEVDKQVVGISVYLWIMLIFLLNVNGWYVYIWTIVPFIIM  
301

360



FIGURE 1D

SEQ ID NO:41 LIAVGTKLEHVIAOLAHEVAEKHVAIEGDLVVKPSDEHFWFSKPQIVLYLIHFILFQNAF  
SEQ ID NO:40 LIAVGTKLOATMAMALEIVEETHAVVOGMPVQGSDDRYFEDCPQLLLHLIHFALFQNAF  
SEQ ID NO:39 LLCVGTKLEMIIMEMALEIQDRASVIKGPVVEPSNKEFFWHRPDWVLFHILTLFQNAF  
SEQ ID NO:42 LIIIVGTKLQVITIKGLRIQEKGDVVKGTPLVQPGDHFHFEGRPRFLFHLIHLFTNAF  
SEQ ID NO:08 LIAVGTKLEHIIITOLAHEVPEKHAATEGDLVQPSDEHFWHRPHVVLFIHLIFLQNAF  
SEQ ID NO:12 LIAVGTKLOAILANMALEITEERHNAVVOGMPVQGSDDRYFEGQQLVLIHLIHFALFQNAF  
SEQ ID NO:14 -----  
SEQ ID NO:28 -----  
SEQ ID NO:32 LLCVGTKLEMIIMEMALEIQDRASVIKGPVVEPSNKEFFWHRPDWVLFHILTLFQNAF  
SEQ ID NO:38 LLMVGSKEHIIITELAYEVAQKHTAIRGDLVSPSDNFFWHRPKLVLLIHLIHLIFLQNAF  
420  
361  
SEQ ID NO:41 EIAFFFWIIVWYGFDSICMGQVRYIVPRLVIGVFIQVLCYSYSTLPYALVVSOMGSSFFKA  
SEQ ID NO:40 QITHFHWISYGLKSCFHKDFNLVSVSKJFLCLGALILCSYITITPLVALVTQMSHMKKA  
SEQ ID NO:39 QMAHFVMTVATPGLKKYHTQIGLSIMKVVGLAQFLCSYMTFPLVALVTQMSNNKRS  
SEQ ID NO:42 QLAFFWSTYFGLKNCFHESRDVIRISIGLLVQLCSYVTLPLVALVTQMSRMKPT  
SEQ ID NO:08 EIAFFFWIIVWYGFDSICMGQVRYIVPRLVIGVFIQVLCYSYSTLPYALVTQMGTHYKRA  
SEQ ID NO:12 QITYILWISYFGLRNCFRDYLAVVVKALXM-MLCJCSYITITPLVALVTQMSNNKTA  
SEQ ID NO:14 -----  
SEQ ID NO:28 -----FFA-----  
SEQ ID NO:32 QMAHFVMTVATPGLKKCFHMHIGLSIMKVVGLAQFLCSYITFPLVALVTQMSNNKRS  
SEQ ID NO:38 EIAFFFWIIVWYGFDSICMGQVRYIVPRLVISVICOVLCGYSTLPYALVVSOMGSSFFKT  
421  
480



FIGURE 1E

```
SEQ ID No:41 IFENVQVLGVWAKQVKQRDLKAAA-----SNGDESSQAGPGPDSSGSGS-----
SEQ ID No:40 VFDEQMAKALKKWKHKIKLKK-----GKARLPSTKILGVSEFSL-----
SEQ ID No:39 IFDEQTSKALTWNWNTAKEKKKVRDMDLMAQIMIGDATPSRGSSPMPSRGSSPVLHLHKG
SEQ ID No:42 VNERVATALKSWHHTA--KKNIKH-----GRTSESTPFSRRPTPTHGSSPIHLRNA
SEQ ID No:08 IFNDHLQONI VGVWAKQKRRKGLKA-----DGNFGGSSQESAN-----
SEQ ID No:12 IFDEQTNKALKKWHMAAKKQ-----GGAVTLGKSSARIMDGSPI-----
SEQ ID No:14 IFDEQTNKALKKWHMAAKKQ-----KDKKK-----
SEQ ID No:28 IFDEQTNKALKKWHMAAKKQ-----KDKKK-----
SEQ ID No:32 IFDEQTNKALTWNWNTAKEKKKVRDMDLMAQIMIGDATPSRGTSMPSPASSPVLHLHKG
SEQ ID No:38 IFDENVTGLVNWAEKA--RRGTRTEN---KITDASSSPIDEANGGA-----
481
SEQ ID No:41 -----APAAGCGAGFAGIQLSRVTRNNAGDTNNEITPDHN-----N-----
SEQ ID No:40 -----SSSSSATLLHRSKTTGH---SSNIIYKQDEEDEMDS--L-----
SEQ ID No:39 -----MGRSDD-----PQSAPTSPTQOEADMYPVVVAHPVHRLNPNDRRRSSASSAL
SEQ ID No:42 PHKRSRVSDESFANSFSPRNSDFSDWDPESQHETAETSNNSHRSRTEGESEKKEKVVSSV
SEQ ID No:08 -----TGQLGSIFFKATAPAGDSSAPKADGICISV-----
SEQ ID No:12 -----GNSSTVHSLAPHYTVSKLATQAPAHQOQTRIKIKIMN--M-----
SEQ ID No:14 -----K-----
SEQ ID No:28 -----MGRSDD-----PQSAPTSPTMEEARADMYPVVVAHPVHRLNPNDRRRSSASSAL
SEQ ID No:32 -----MGRSDD-----PQSAPTSPTMEEARADMYPVVVAHPVHRLNPNDRRRSSASSAL
SEQ ID No:38 -----VQMT-----NTRANSVEQGTARLI.-----
541
600
```



**FIGURE 1F**

```
SEQ ID NO:41 -----  
SEQ ID NO:40 EAGAEDAIDRIQQEQMF-----HNS  
SEQ ID NO:39 E-----ADIPSADFSQ-G  
SEQ ID NO:42 ELPPGPGQIRTOHEISTISLRDFSFKR--  
SEQ ID NO:08 -----  
SEQ ID NO:12 NPMVLSCLRWRKQOASL.-----  
SEQ ID NO:14 -----  
SEQ ID NO:28 -----  
SEQ ID NO:32 D-----ADIPSADFSQG.  
SEQ ID NO:38 -----  
601  
629
```